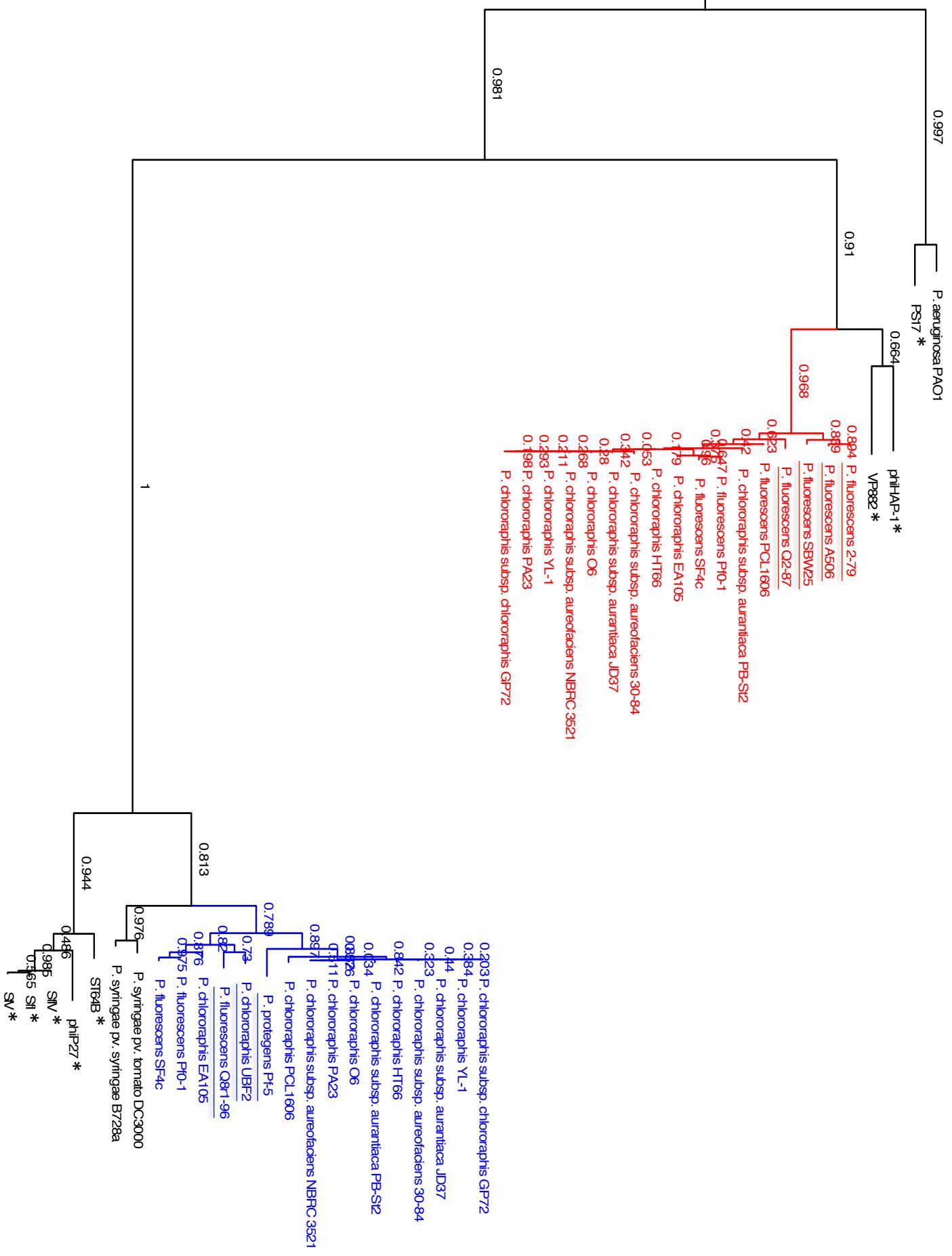


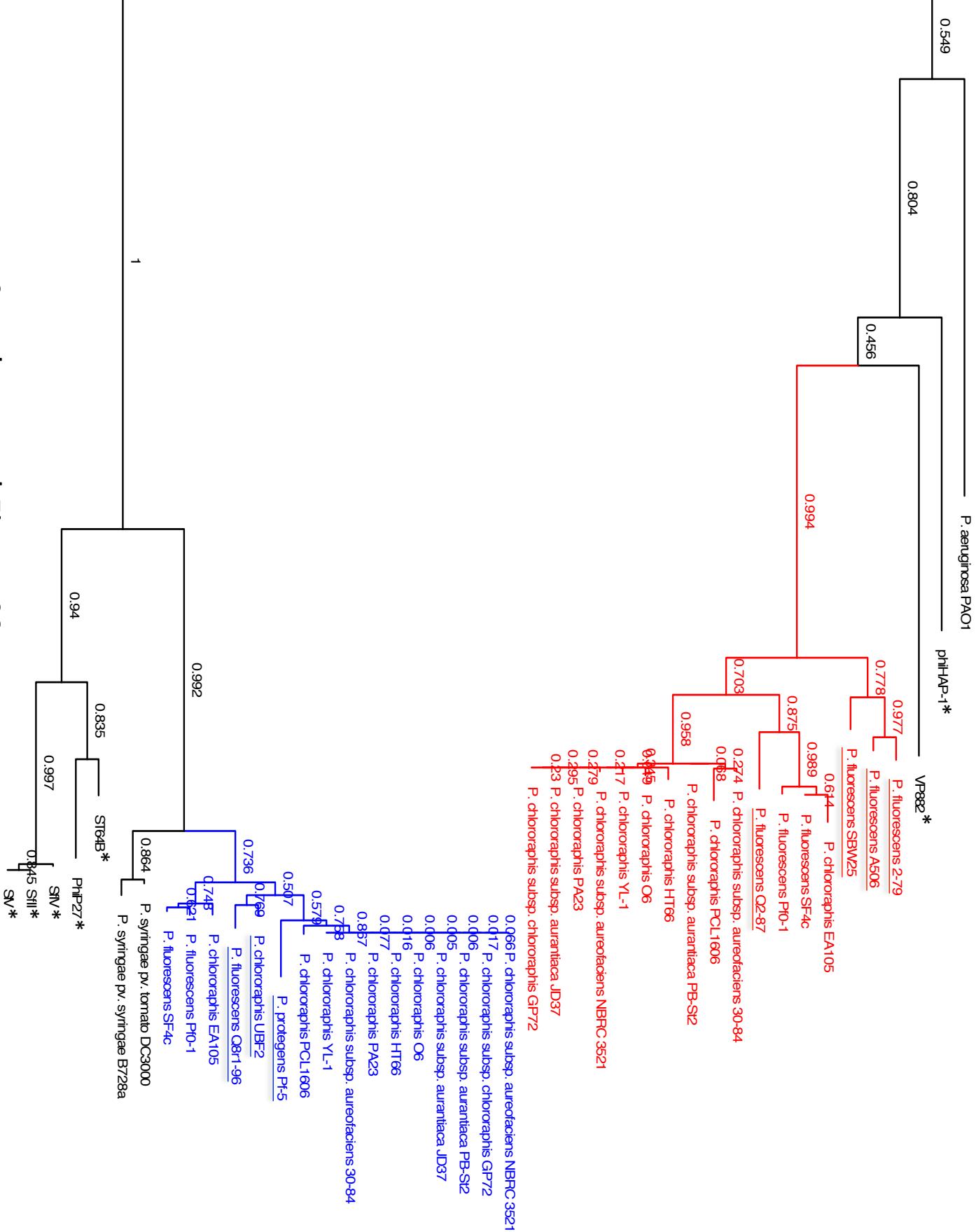
Supplemental Figure S1



Supplemental Figure S2

Supplemental Figure S3

P2*



Supplemental Figure Legends

Supplemental Figure 1: Phylogenetic analysis of tail tube proteins. The maximum likelihood tree was constructed from a multiple sequence alignment (MUSCLE) of the amino acid sequence of tail tube protein homologs from *Pseudomonas* R-tailocin clusters as well as select bacteriophage genomes (denoted by black with asterisks). The two *P. chlororaphis* 30-84 tailocins cluster separately: the tail tube sequences from the tailocin gene region designated tailocin 1 (red) cluster with some strains also encoding two tailocin particles (red) as well as some encoding only one tailocin particle (red underlined). The tail tube sequences from the region designated tailocin 2 cluster together with strains encoding two (blue) or one tailocin particle (blue underlined). Sequences from *P. aeruginosa* PAO1 and a few phyllosphere-colonizing *P. syringae* strains with tailocin clusters are shown for comparison (black). The scale bar represents the number of AA substitutions per site. Bootstrap values (percent of 1,000 replications) are at branches.

Supplemental Figure 2: Phylogenetic analysis of sheath proteins. The maximum likelihood tree was constructed from a multiple sequence alignment (MUSCLE) of the amino acid sequence of sheath protein homologs. The labeling scheme is the same as in S1.

Supplemental Figure 3: Phylogenetic analysis of baseplate spike proteins. The maximum likelihood tree was constructed from a multiple sequence alignment (MUSCLE) of the amino acid sequence of baseplate spike protein homologs. The labeling scheme is the same as in S1.